

# SEQ SEARCH SUMMARY

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 27, 2004, 16:24:09 ; Search time 5680 Seconds  
(without alignments)  
6503.184 Million cell updates/sec

Title: US-09-976-059A-15  
Perfect score: 44310  
Sequence: 1 MIPLSFAQRRLWFLGRLEGP.....DMLALLWPAVEAWQAGRHRP 8695

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09976059/runat\_25032004\_135556\_5662/app\_query.fasta\_1.88  
39

-DB=N\_Geneseq\_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09976059\_@CGN\_1\_1\_4693\_@runat\_25032004\_135556\_5662 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	43400	97.9	88421	6	AAL40781	Aal40781 88421nt g
	2	14882	33.6	110000	7	ACF67367_03	Continuation (4 of
	3	14784	33.4	110000	7	ACF65383_2	Continuation (3 of
	4	14373.5	32.4	31737	7	ACF67733	Acf67733 Photorhab
	5	13862.5	31.3	90600	6	ABQ78872	Abq78872 S. roseos
	6	13014.5	29.4	31263	7	ACA37577	Aca37577 Prokaryot
	7	11069.5	25.0	110000	7	ACF65383_3	Continuation (4 of
	8	10137	22.9	110000	7	ACF67367_50	Continuation (51 o
	9	10137	22.9	110000	7	ACF65387_1	Continuation (2 of
	10	9753	22.0	100779	7	ACF65386_6	Continuation (7 of
c	11	9753	22.0	110000	7	ACF67367_22	Continuation (23 o
	12	8814	19.9	96798	7	ACF65387_6	Continuation (7 of
	13	8355	18.9	15651	7	ACF72072	Acf72072 Photorhab
	14	8355	18.9	110000	7	ACF67367_52	Continuation (53 o
	15	8355	18.9	110000	7	ACF65387_4	Continuation (5 of
	16	8261.5	18.6	47988	9	ADE86070	Ade86070 Streptomy
	17	8018	18.1	31122	2	AAQ40706	Aaq40706 Bacillus
	18	7892.5	17.8	16374	7	ACF72217	Acf72217 Photorhab
	19	7892.5	17.8	110000	7	ACF67367_55	Continuation (56 o
	20	7811	17.6	58857	3	AAA58471	Aaa58471 Nucleotid
	21	7578	17.1	46899	2	AAQ54386	Aaq54386 T. niveum
	22	7518	17.0	41599	4	AAI66165	Aai66165 Bacillus
	23	7156.5	16.2	14952	7	ACF69283	Acf69283 Photorhab
	24	5877.5	13.3	15450	7	ACA19579	Aca19579 Prokaryot
	25	4964	11.2	10002	7	ACA26601	Aca26601 Prokaryot
	26	4675	10.6	110000	7	ACF67367_53	Continuation (54 o
	27	4634.5	10.5	10296	7	ACA45795	Aca45795 Prokaryot
	28	4593	10.4	7617	7	ACA37601	Aca37601 Prokaryot
	29	4514	10.2	9936	7	ACF72211	Acf72211 Photorhab
	30	4514	10.2	110000	7	ACF67367_54	Continuation (55 o
	31	4453.5	10.1	18660	3	AAA58472	Aaa58472 Nucleotid
	32	4432.5	10.0	135638	7	ABX34289	Abx34289 S. atrool
	33	4425	10.0	8649	7	ACA38131	Aca38131 Prokaryot
c	34	4386	9.9	110000	4	AAI99682_26	Continuation (27 o
c	35	4364.5	9.8	110000	4	AAI99683_26	Continuation (27 o
	36	4344	9.8	9590	7	ACA45481	Aca45481 Prokaryot
	37	4283.5	9.7	13029	4	AAS51470	Aas51470 Pseudomon
	38	4283.5	9.7	13029	7	ACA19370	Aca19370 Prokaryot
	39	4250.5	9.6	9813	7	ACF71803	Acf71803 Photorhab
c	40	4221.5	9.5	50538	6	ABS78890	Abs78890 E. coli C
c	41	4182.5	9.4	48715	4	ABA89188	Aba89188 Escherich
	42	4178	9.4	9748	7	ACA43518	Aca43518 Prokaryot
	43	4156	9.4	9858	7	ACF71802	Acf71802 Photorhab
	44	4149	9.4	12951	7	ACA43808	Aca43808 Prokaryot
	45	3979.5	9.0	37856	3	AAA11992	Aaa11992 S. cellul

WD 02/31/55

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 27, 2004, 15:34:39 ; Search time 65284 Seconds  
(without alignments)  
5772.742 Million cell updates/sec

Title: US-09-976-059A-15  
Perfect score: 44310  
Sequence: 1 MIPLSFAQRRLWFLGRLEGP.....DMLALLWPAVEAWQAGRHRP 8695

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09976059/runat\_25032004\_135555\_5607/app\_query.fasta\_1.88  
39

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09976059\_@CGN\_1\_1\_45199\_@runat\_25032004\_135555\_5607 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*

11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*  
 15: em\_ba:\*  
 16: em\_fun:\*  
 17: em\_hum:\*  
 18: em\_in:\*  
 19: em\_mu:\*  
 20: em\_om:\*  
 21: em\_or:\*  
 22: em\_ov:\*  
 23: em\_pat:\*  
 24: em\_ph:\*  
 25: em\_pl:\*  
 26: em\_ro:\*  
 27: em\_sts:\*  
 28: em\_un:\*  
 29: em\_vi:\*  
 30: em\_htg\_hum:\*  
 31: em\_htg\_inv:\*  
 32: em\_htg\_other:\*  
 33: em\_htg\_mus:\*  
 34: em\_htg\_pln:\*  
 35: em\_htg\_rod:\*  
 36: em\_htg\_mam:\*  
 37: em\_htg\_vrt:\*  
 38: em\_sy:\*  
 39: em\_htgo\_hum:\*  
 40: em\_htgo\_mus:\*  
 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		Query		%				Description
No.	Score	Match	Length	DB	ID			
c	1	43400	97.9	88421	6	AX417445	GenBank	AX417445 Sequence
	2	14882	33.6	345829	1	BX571868		BX571868 Photorhab
	3	14784	33.4	349980	6	AX770905		AX770905 Sequence
	4	14238.5	32.1	213050	1	AL646079		AL646079 Ralstonia
	5	13939.5	31.5	276800	1	SCO939115		AL939115 Streptomy
	6	13547.5	30.6	310029	1	AE016866		AE016866 Pseudomon
	7	13469	30.4	40430	1	AB107223		AB107223 Pseudomon
	8	13250.5	29.9	61944	6	AX803750		AX803750 Sequence
	9	13120	29.6	73800	1	AF286216		AF286216 Pseudomon
	10	12879	29.1	37360	6	AX803722		AX803722 Sequence
	11	12737	28.7	28587	1	AF047828		AF047828 Pseudomon
	12	11209	25.3	22449	1	SPSNBCDE		Y11548 S.pristinae
	13	11209	25.3	22449	1	SPSNBCGEN		X98690 S.pristinae
	14	10881.5	24.6	40989	1	AF204805		AF204805 Nostoc sp
	15	10205.5	23.0	34328	1	AY167420		AY167420 Nostoc sp
	16	10167.5	22.9	40897	1	AF004835		AF004835 Brevibaci

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 27, 2004, 19:08:38 ; Search time 5215 Seconds  
(without alignments)  
6207.396 Million cell updates/sec

Title: US-09-976-059A-15  
Perfect score: 44310  
Sequence: 1 MIPLSFAQRRLWFLGRLEGP.....DMLALLWPAVEAWQAGRHRP 8695

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 2458946 seqs, 1861504846 residues

Total number of hits satisfying chosen parameters: 4917892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

Q=/cgn2\_1/USPTO\_spool/US09976059/runat\_25032004\_135556\_5673/app\_query.fasta\_1.88  
39

-DB=Published\_Applications\_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09976059\_@CGN\_1\_1\_2279\_@runat\_25032004\_135556\_5673  
-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
 16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
 17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
 18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43400	97.9	88421	9	US-09-976-059-1	Sequence 1, Appli
2	13250.5	29.9	61944	14	US-10-329-079-34	Sequence 34, Appl
3	13014.5	29.4	31263	12	US-10-282-122A-25447	Sequence 25447, A
4	12879	29.1	37360	14	US-10-329-079-6	Sequence 6, Appli
5	8558.5	19.3	18876	14	US-10-329-079-42	Sequence 42, Appl
6	8261.5	18.6	47988	15	US-10-402-842-1	Sequence 1, Appli
7	8114	18.3	15738	14	US-10-329-079-46	Sequence 46, Appl
8	7847	17.7	15738	14	US-10-329-079-12	Sequence 12, Appl
c 9	7348	16.6	9025608	14	US-10-156-761-1	Sequence 1, Appli
10	5877.5	13.3	15450	12	US-10-282-122A-7449	Sequence 7449, Ap
11	5155.5	11.6	13315	14	US-10-329-079-1	Sequence 1, Appli
12	4964	11.2	10002	12	US-10-282-122A-14471	Sequence 14471, A
13	4844.5	10.9	11058	14	US-10-156-761-3629	Sequence 3629, Ap
14	4834.5	10.9	11100	14	US-10-329-079-5	Sequence 5, Appli
15	4634.5	10.5	10296	12	US-10-282-122A-33665	Sequence 33665, A
16	4593	10.4	7617	12	US-10-282-122A-25471	Sequence 25471, A
17	4432.5	10.0	135638	14	US-10-314-657-1	Sequence 1, Appli
18	4425	10.0	8649	12	US-10-282-122A-26001	Sequence 26001, A
19	4423.5	10.0	7788	14	US-10-329-079-8	Sequence 8, Appli
20	4344	9.8	9590	12	US-10-282-122A-33351	Sequence 33351, A
21	4308.5	9.7	8244	15	US-10-402-842-3	Sequence 3, Appli
22	4283.5	9.7	13029	9	US-09-815-242-4052	Sequence 4052, Ap
23	4283.5	9.7	13029	12	US-10-282-122A-7240	Sequence 7240, Ap
c 24	4221.5	9.5	50538	14	US-10-085-959-57	Sequence 57, Appl
c 25	4182.5	9.4	48715	14	US-10-238-075-921	Sequence 921, App
26	4178	9.4	9748	12	US-10-282-122A-31388	Sequence 31388, A
27	4149	9.4	12951	12	US-10-282-122A-31678	Sequence 31678, A
28	4069	9.2	7185	14	US-10-329-079-48	Sequence 48, Appl
29	4054.5	9.2	7155	14	US-10-329-079-14	Sequence 14, Appl
30	4025	9.1	11007	15	US-10-402-842-5	Sequence 5, Appli
31	3751	8.5	9399	15	US-10-369-493-42604	Sequence 42604, A
32	3730	8.4	7158	9	US-09-974-300-2171	Sequence 2171, Ap
33	3592	8.1	6432	14	US-10-329-079-10	Sequence 10, Appl
34	3567.5	8.1	6408	14	US-10-329-079-44	Sequence 44, Appl
35	3567.5	8.1	9683	15	US-10-369-493-38492	Sequence 38492, A
36	3410	7.7	7155	12	US-10-282-122A-10403	Sequence 10403, A
37	3375	7.6	9723	12	US-10-282-122A-13740	Sequence 13740, A
38	3325.5	7.5	7347	9	US-09-815-242-7773	Sequence 7773, Ap
39	3325.5	7.5	7347	12	US-10-282-122A-7467	Sequence 7467, Ap

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 27, 2004, 16:21:54 ; Search time 981 Seconds  
(without alignments)  
4918.754 Million cell updates/sec

Title: US-09-976-059A-15  
Perfect score: 44310  
Sequence: 1 MIPLSFAQRRLWFLGRLEGP.....DMLALLWPAVEAWQAGRHRP 8695

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlh

-

Q=/cgn2\_1/USPTO\_spool/US09976059/runat\_25032004\_135555\_5615/app\_query.fasta\_1.88  
39

-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09976059\_@CGN\_1\_1\_487\_@runat\_25032004\_135555\_5615 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query					ID	Description
	No.	Score	Match	Length	DB		
	1	7582	17.1	46899	1	US-08-471-119A-1	Sequence 1, Appli
c	2	4386	9.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	3	4364.5	9.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	4	3333	7.5	7374	4	US-09-252-991A-9100	Sequence 9100, Ap
	5	3298.5	7.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	6	3293	7.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	7	3278	7.4	10023	4	US-09-252-991A-6997	Sequence 6997, Ap
	8	3124.5	7.1	11601	2	US-08-222-617A-3	Sequence 3, Appli
	9	3124.5	7.1	11601	2	US-08-222-617A-24	Sequence 24, Appl
	10	3056	6.9	7911	4	US-09-252-991A-9182	Sequence 9182, Ap
	11	2991.5	6.8	7527	4	US-09-252-991A-71	Sequence 71, Appl
	12	2916.5	6.6	12364	2	US-08-222-617A-1	Sequence 1, Appli
	13	2905	6.6	11444	2	US-08-222-617A-26	Sequence 26, Appl
	14	2894.5	6.5	6573	4	US-09-252-991A-9183	Sequence 9183, Ap
	15	2890	6.5	77536	4	US-09-410-551B-1	Sequence 1, Appli
	16	2466	5.6	6858	4	US-09-252-991A-1219	Sequence 1219, Ap
c	17	1897.5	4.3	3315	4	US-09-252-991A-8892	Sequence 8892, Ap
	18	1897.5	4.3	7215	4	US-09-134-001C-627	Sequence 627, App
c	19	1825	4.1	29555	4	US-08-956-171E-206	Sequence 206, App
	20	1793.5	4.0	68750	3	US-09-335-409-1	Sequence 1, Appli
	21	1793.5	4.0	68750	4	US-09-568-102-1	Sequence 1, Appli
	22	1793.5	4.0	68750	4	US-09-567-969-1	Sequence 1, Appli
	23	1793.5	4.0	68750	4	US-09-568-480-1	Sequence 1, Appli
	24	1793.5	4.0	68750	4	US-09-568-486-1	Sequence 1, Appli
	25	1793.5	4.0	68750	4	US-09-568-472-1	Sequence 1, Appli
	26	1793.5	4.0	68750	4	US-09-567-899-1	Sequence 1, Appli
	27	1781	4.0	2219	3	US-08-510-646B-17	Sequence 17, Appl
	28	1757	4.0	71989	4	US-09-443-501A-2	Sequence 2, Appli
c	29	1714.5	3.9	4242	4	US-09-252-991A-7056	Sequence 7056, Ap
c	30	1625	3.7	4236	4	US-09-252-991A-7057	Sequence 7057, Ap
c	31	1595	3.6	77536	4	US-09-410-551B-1	Sequence 1, Appli
	32	1509.5	3.4	44377	2	US-08-804-227C-7	Sequence 7, Appli
	33	1509.5	3.4	44377	2	US-08-804-198-1	Sequence 1, Appli
	34	1471	3.3	47981	4	US-09-679-279-1	Sequence 1, Appli
	35	1445	3.3	38506	3	US-09-320-878-19	Sequence 19, Appl
	36	1445	3.3	38506	4	US-09-141-908-1	Sequence 1, Appli
	37	1445	3.3	38506	4	US-09-657-440-19	Sequence 19, Appl
	38	1440.5	3.3	43280	2	US-08-804-227C-1	Sequence 1, Appli
	39	1395	3.1	36778	3	US-09-105-537-5	Sequence 5, Appli
c	40	1362.5	3.1	53500	4	US-09-266-965-76	Sequence 76, Appl
	41	1334	3.0	50937	3	US-09-428-517-1	Sequence 1, Appli
	42	1330	3.0	3915	4	US-09-489-039A-6278	Sequence 6278, Ap
	43	1327.5	3.0	80161	3	US-09-036-987A-1	Sequence 1, Appli
	44	1327.5	3.0	80161	3	US-09-370-700-1	Sequence 1, Appli
	45	1327.5	3.0	80161	4	US-09-603-207-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1

US-08-471-119A-1